AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

Claims 1-9 (Canceled).

10. (Currently Amended) A purified polypeptide encoded by a nucleic acid molecule selected from the group comprising

(A) a purified nucleic acid molecule of sequence SEQ ID NO: 2;

(B) a purified nucleic acid molecule encoding the amino acid sequence SEQ ID NO: 1;

(C) a purified nucleic acid molecule degenerate from SEQ ID NO: 2 as a result of the genetic code; or

(D) a purified nucleic acid molecule that encodes a core+1 polypeptide~~, an allelic~~ or a variant of core+1 polypeptide~~, or a homolog of core+1 polypeptide~~, wherein the variant is detectable by Western analysis using HCV-positive human serum or monoclonal antibody against core protein, and wherein the amino acid sequence of the variant shares at least 80% identity with a native core+1 polypeptide amino acid sequence.

11. (Original) A purified polypeptide according to claim 10 having a molecular weight of approximately 17.5 kD as determined by SDS-PAGE.

12. (Original) A purified polypeptide according to claim 10 in non-glycosylated form.

13. (Currently Amended) A purified polypeptide encoded by~~ a nucleic acid molecule of claim 3~~:

(A) a purified nucleic acid molecule that hybridizes to either strand of a denatured, double-stranded DNA comprising the nucleic acid sequence of SEQ ID NO: 2; or

(B) a purified nucleic acid molecule that hybridizes to either strand of a denatured, double-stranded DNA comprising the nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 1;

wherein the conditions for hybridization are 50% formamide and 6X SSC, at 42°C with washing conditions of 60°C, 0.5X SSC, 0.1% SDS.

14. (Original) A purified polypeptide according to claim 13 in non-glycosylated form.

15. (Currently Amended) A purified polypepetide encoded by ~~a nucleic acid molecule of claim 4.~~

(A) a purified nucleic acid molecule that hybridizes to either strand of a denatured, double-stranded DNA comprising the nucleic acid sequence of SEQ ID NO: 2; or

(B) a purified nucleic acid molecule that hybridizes to either strand of a denatured, double-stranded DNA comprising the nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 1;

wherein the conditions for hybridization are 50% formamide and 6X SSC, at 42°C with washing conditions of 60°C, 0.5X SSC, 0.1% SDS;

and further, wherein said purified nucleic acid molecule is derived by *in vitro* mutagenesis from SEQ ID NO: 2; the resulting mutant variant of core+1 polypeptide is detectable by Western analysis using HCV-positive human serum or monoclonal

antibody against core protein; and the amino acid sequence of the resulting mutant variant shares at least 80% identity with a native core+1 polypeptide amino acid sequence.

16. (Original) A purified polypeptide according to claim 15 in non-glycosylated form.

17. (Original) Purified antibodies that bind to a polypeptide of claim 10.

18. (Original) Purified antibodies according to claim 17, wherein the antibodies are monoclonal antibodies.

19. (Original) Purified antibodies that bind to a polypeptide of claim 13.

20. (Original) Purified antibodies according to claim 19, wherein the antibodies are monoclonal antibodies.

21. (Original) Purified antibodies that bind to a polypeptide of claim 15.

22. (Original) Purified antibodies according to claim 21, wherein the antibodies are monoclonal antibodies.

Claims 23 -32 (Canceled).

33. (Original) An immunological complex comprising a core+1 polypeptide of HCV and an antibody that specifically recognizes said polypeptide.

34. (Withdrawn) A method for detecting infection by hepatitis C virus (HCV), wherein the method comprises providing a composition comprising a biological material suspected of being infected with HCV, and assaying for the presence of core+1 polypeptide of HCV.

35. (Withdrawn) The method as claimed in claim 34, wherein the core+1 polypeptide is assayed by electrophoresis or by immunoassay with antibodies that are immunologically reactive with the core+1 polypeptide.

36. (Withdrawn) An *in vitro* diagnostic method for detection of the presence or absence of antibodies, which bind to an antigen comprising core+1 polypeptide, wherein the method comprises contacting the antigen with a biological fluid for a time and under conditions sufficient for the antigen and antibodies in the biological fluid to form an antigen-antibody complex, and detecting the formation of the complex.

37. (Withdrawn) The method as claimed in claim 36, which further comprises measuring the formation of the antigen-antibody complex.

38. (Withdrawn) The method as claimed in claim 36, wherein the formation of antigen-antibody complex is detected by immunoassay based on Western blot technique, ELISA, indirect immuno-fluorescence assay, or immunoprecipitation assay.

39. (Withdrawn) A diagnostic kit for the detection of the presence or absence of antibodies, which bind to core+1 polypeptide or mixtures thereof, wherein the kit comprises an antigen comprising core+1 polypeptide or mixtures of core+1 polypeptides, and means for detecting the formation of immune complex between the antigen and antibodies, wherein the means are present in an amount sufficient to perform said detection.

Claims 40-41 (Canceled).

42. (Withdrawn) A method for detecting the presence or absence of hepatitis C virus (HCV) comprising:

(1) contacting a sample suspected of containing viral genetic material of HCV with at least one nucleotide probe, and

(2) detecting hybridization between the nucleotide probe and the viral genetic material in the sample,

wherein said nucleotide probe is complementary to the full-length sequence of the purified nucleic acid of SEQ ID NO: 2.

43. (New) A purified polypeptide according to claim 10, wherein the amino acid sequence of the variant shares at least 90% identity with a native core+1 polypeptide amino acid sequence.

44. (New) A purified polypeptide according to claim 15, wherein the amino acid sequence of the resulting mutant variant shares at least 90% identity with a native core+1 polypeptide amino acid sequence.